

ENTERED



PCT09

RAW SEQUENCE LISTING

DATE: 07/12/2002

PATENT APPLICATION: US/09/936,035

TIME: 11:16:52

Input Set : N:\Crf3\Datahold\EFS\09936035\gncap01005.txt

Output Set: N:\CRF3\07122002\I936035.raw

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3 <110> APPLICANT: Genetica, Inc.
4     Beach, David H.
5     Hannon, Gregory J.
7 <120> TITLE OF INVENTION: METHODS AND REAGENTS FOR INCREASING PROLIFERATIVE
8     CAPACITY AND PREVENTING REPLICATIVE SENESENCE
10 <130> FILE REFERENCE: GNCA-P01-005
12 <140> CURRENT APPLICATION NUMBER: 09/936,035
13 <141> CURRENT FILING DATE: 1999-11-24
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/27907
16 <151> PRIOR FILING DATE: 1999-11-24
18 <150> PRIOR APPLICATION NUMBER: 60/120,549
19 <151> PRIOR FILING DATE: 1999-02-17
21 <150> PRIOR APPLICATION NUMBER: 60/109,891
22 <151> PRIOR FILING DATE: 1998-11-25
24 <160> NUMBER OF SEQ ID NOS: 43
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 4027
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (57)..(3452)
37 <400> SEQUENCE: 1
38 caggcagcgt ggtcctgctg cgcacgtggg aagccctggc cccggccacc cccgcg atg 59
39                                     Met
40                                     1
42 ccg cgc gct ccc cgc tgc cga gcc gtg cgc tcc ctg ctg cgc agc cac 107
43 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
44         5                10                15
46 tac cgc gag gtg ctg ccg ctg gcc acg ttc gtg cgg cgc ctg ggg ccc 155
47 Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
48         20                25                30
50 cag ggc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc gcg 203
51 Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
52         35                40                45
54 ctg gtg gcc cag tgc ctg gtg tgc gtg ccc tgg gac gca cgg ccg ccc 251
55 Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
56 50                55                60                65
58 ccc gcc gcc ccc tcc ttc cgc cag gtg tcc tgc ctg aag gag ctg gtg 299
59 Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
60         70                75                80
62 gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg ctg 347

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63 Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu
64      85      90      95
66 gcc ttc ggc ttc gcg ctg ctg gac ggg gcc cgc ggg ggc ccc ccc gag 395
67 Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu
68      100      105      110
70 gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc gac 443
71 Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp
72      115      120      125
74 gca ctg cgg ggg agc ggg gcg tgg ggg ctg ctg ttg cgc cgc gtg ggc 491
75 Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly
76 130      135      140      145
78 gac gac gtg ctg gtt cac ctg ctg gca cgc tgc gcg ctc ttt gtg ctg 539
79 Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu
80      150      155      160
82 gtg gct ccc agc tgc gcc tac cag gtg tgc ggg ccg ccg ctg tac cag 587
83 Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln
84      165      170      175
86 ctc ggc gct gcc act cag gcc cgg ccc ccg cca cac gct agt gga ccc 635
87 Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro
88      180      185      190
90 cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg gag 683
91 Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu
92      195      200      205
94 gcc ggg gtc ccc ctg ggc ctg cca gcc ccg ggt gcg agg agg cgc ggg 731
95 Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly
96 210      215      220      225
98 ggc agt gcc agc cga agt ctg ccg ttg ccc aag agg ccc agg cgt ggc 779
99 Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly
100      230      235      240
102 gct gcc cct gag ccg gag cgg acg ccc gtt ggg cag ggg tcc tgg gcc 827
103 Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala
104      245      250      255
106 cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg gtg 875
107 His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val
108      260      265      270
110 tca cct gcc aga ccc gcc gaa gaa gcc acc tct ttg gag ggt gcg ctc 923
111 Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu
112      275      280      285
114 tct ggc acg cgc cac tcc cac cca tcc gtg ggc cgc cag cac cac gcg 971
115 Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala
116 290      295      300      305
118 ggc ccc cca tcc aca tcg cgg cca cca cgt ccc tgg gac acg cct tgt 1019
119 Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys
120      310      315      320
122 ccc ccg gtg tac gcc gag acc aag cac ttc ctc tac tcc tca ggc gac 1067
123 Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp
124      325      330      335
126 aag gag cag ctg cgg ccc tcc ttc cta ctc agc tct ctg agg ccc agc 1115
127 Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser

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128				340			345			350							
130	ctg	act	ggc	gct	cgg	agg	ctc	gtg	gag	acc	atc	ttt	ctg	ggt	tcc	agg	1163
131	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	
132	355						360			365							
134	ccc	tgg	atg	cca	ggg	act	ccc	cgc	agg	ttg	ccc	cgc	ctg	ccc	cag	cgc	1211
135	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	
136	370						375			380			385				
138	tac	tgg	caa	atg	cgg	ccc	ctg	ttt	ctg	gag	ctg	ctt	ggg	aac	cac	gcg	1259
139	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
140				390						395			400				
142	cag	tgc	ccc	tac	ggg	gtg	ctc	ctc	aag	acg	cac	tgc	ccg	ctg	cga	gct	1307
143	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
144				405						410			415				
146	gcg	gtc	acc	cca	gca	gcc	ggt	gtc	tgt	gcc	cgg	gag	aag	ccc	cag	ggc	1355
147	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
148	420						425						430				
150	tct	gtg	gcg	gcc	ccc	gag	gag	gag	gac	aca	gac	ccc	cgt	cgc	ctg	gtg	1403
151	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
152	435						440						445				
154	cag	ctg	ctc	cgc	cag	cac	agc	agc	ccc	tgg	cag	gtg	tac	ggc	ttc	gtg	1451
155	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
156	450						455						460			465	
158	cgg	gcc	tgc	ctg	cgc	cgg	ctg	gtg	ccc	cca	ggc	ctc	tgg	ggc	tcc	agg	1499
159	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
160				470						475						480	
162	cac	aac	gaa	cgc	cgc	ttc	ctc	agg	aac	acc	aag	aag	ttc	atc	tcc	ctg	1547
163	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
164				485						490						495	
166	ggg	aag	cat	gcc	aag	ctc	tcg	ctg	cag	gag	ctg	acg	tgg	aag	atg	agc	1595
167	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
168	500						505						510				
170	gtg	cgg	ggc	tgc	gct	tgg	ctg	cgc	agg	agc	cca	ggg	ggt	ggc	tgt	gtt	1643
171	Val	Arg	Gly	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
172	515						520						525				
174	ccg	gcc	gca	gag	cac	cgt	ctg	cgt	gag	gag	atc	ctg	gcc	aag	ttc	ctg	1691
175	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
176	530						535						540			545	
178	cac	tgg	ctg	atg	agt	gtg	tac	gtc	gtc	gag	ctg	ctc	agg	tct	ttc	ttt	1739
179	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
180				550						555						560	
182	tat	gtc	acg	gag	acc												

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194 cgg gaa gcc agg ccc gcc ctg ctg acg tcc aga ctc cgc ttc atc ccc 1931
195 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
196 610 615 620 625
198 aag cct gac ggg ctg cgg ccg att gtg aac atg gac tac gtc gtg gga 1979
199 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
200 630 635 640
202 gcc aga acg ttc cgc aga gaa aag agg gcc gag cgt ctc acc tcg agg 2027
203 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
204 645 650 655
206 gtg aag gca ctg ttc agc gtg ctc aac tac gag cgg gcg cgg cgc ccc 2075
207 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
208 660 665 670
210 ggc ctc ctg ggc gcc tct gtg ctg ggc ctg gac gat atc cac agg gcc 2123
211 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
212 675 680 685
214 tgg cgc acc ttc gtg ctg cgt gtg cgg gcc cag gac ccg ccg cct gag 2171
215 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
216 690 695 700 705
218 ctg tac ttt gtc aag gtg gat gtg acg ggc gcg tac gac acc atc ccc 2219
219 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
220 710 715 720
222 cag gac agg ctc acg gag gtc atc gcc agc atc atc aaa ccc cag aac 2267
223 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
224 725 730 735
226 acg tac tgc gtg cgt cgg tat gcc gtg gtc cag aag gcc gcc cat ggg 2315
227 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
228 740 745 750
230 cac gtc cgc aag gcc ttc aag agc cac gtc tct acc ttg aca gac ctc 2363
231 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
232 755 760 765
234 cag ccg tac atg cga cag ttc gtg gct cac ctg cag gag acc agc ccg 2411
235 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro
236 770 775 780 785
238 ctg agg gat gcc gtc gtc atc gag cag agc tcc tcc ctg aat gag gcc 2459
239 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
240 790 795 800
242 agc agt ggc ctc ttc gac gtc ttc cta cgc ttc atg tgc cac cac gcc 2507
243 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
244 805 810 815
246 gtg cgc atc agg ggc aag tcc tac gtc cag tgc cag ggg atc ccg cag 2555
247 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
248 820 825 830
250 ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac atg 2603
251 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
252 835 840 845
254 gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg cgt 2651
255 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
256 850 855 860 865
258 ttg gtg gat gat ttc ttg ttg gtg aca cct cac ctc acc cac gcg aaa 2699

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259	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
260					870					875					880		
262	acc	ttc	ctc	agg	acc	ctg	gtc	cga	ggt	gtc	cct	gag	tat	ggc	tgc	gtg	2747
263	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
264				885					890					895			
266	gtg	aac	ttg	cgg	aag	aca	gtg	gtg	aac	ttc	cct	gta	gaa	gac	gag	gcc	2795
267	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	
268			900					905					910				
270	ctg	ggt	ggc	acg	gct	ttt	gtt	cag	atg	ccg	gcc	cac	ggc	cta	ttc	ccc	2843
271	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	
272		915					920					925					
274	tgg	tgc	ggc	ctg	ctg	ctg	gat	acc	cgg	acc	ctg	gag	gtg	cag	agc	gac	2891
275	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	
276	930					935					940					945	
278	tac	tcc	agc	tat	gcc	cgg	acc	tcc	atc	aga	gcc	agt	ctc	acc	ttc	aac	2939
279	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	Asn	
280					950					955					960		
282	cgc	ggc	ttc	aag	gct	ggg	agg	aac	atg	cgt	cgc	aaa	ctc	ttt	ggg	gtc	2987
283	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	
284				965					970					975			
286	ttg	cgg	ctg	aag	tgt	cac	agc	ctg	ttt	ctg	gat	ttg	cag	gtg	aac	agc	3035
287	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser	
288			980					985					990				
290	ctc	cag	acg	gtg	tgc	acc	aac	atc	tac	aag	atc	ctc	ctg	ctg	cag	gcg	3083
291	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln	Ala	
292		995					1000					1005					
294	tac	agg	ttt	cac	gca	tgt	gtg	ctg	cag	ctc	cca	ttt	cat	cag	caa	gtt	3131
295	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	Phe	His	Gln	Gln	Val	
296	1010				1015					1020					1025		
298	tgg	aag	aac	ccc	aca	ttt	ttc	ctg	cgc	gtc	atc	tct	gac	acg	gcc	tcc	3179
299	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile	Ser	Asp	Thr	Ala	Ser	
300				1030					1035					1040			
302	ctc	tgc	tac	tcc	atc	ctg	aaa	gcc	aag	aac	gca	ggg	atg	tcg	ctg	ggg	3227
303	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala	Gly	Met	Ser	Leu	Gly	
304				1045					1050					1055			
306	gcc	aag	ggc	gcc	gcc	ggc	cct	ctg	ccc	tcc	gag	gcc	gtg	cag	tgg	ctg	3275
307	Ala	Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro	Ser	Glu	Ala	Val	Gln	Trp	Leu	
308			1060				1065						1070				
310	tgc	cac	caa	gca	ttc	ctg	ctc	aag	ctg	act	cga	cac	cgt	gtc	acc	tac	3323
311	Cys	His	Gln	Ala	Phe	Leu	Leu	Lys	Leu	Thr	Arg	His	Arg	Val	Thr	Tyr	
312		1075					1080				1085						
314	gtg	cca	ctc	ctg	ggg	tca	ctc	agg	aca	gcc	cag	acg	cag	ctg	agt	cgg	3371
315	Val	Pro	Leu	Leu	Gly	Ser	Leu	Arg	Thr	Ala	Gln	Thr	Gln	Leu	Ser	Arg	
316	1090				1095					1100					1105		
318	aag	ctc	ccg	ggg	acg	acg	ctg	act	gcc	ctg	gag	gcc	gca	gcc	aac	ccg	3419
319	Lys	Leu	Pro	Gly	Thr	Thr	Leu	Thr	Ala	Leu	Glu	Ala	Ala	Ala	Asn	Pro	
320				1110					1115					1120			
322	gca	ctg	ccc	tca	gac	ttc	aag	acc	atc	ctg	gac	tgatggccac	ccgcccacag				3472
323	Ala	Leu	Pro	Ser	Asp	Phe	Lys	Thr	Ile	Leu	Asp						

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2320,2321,2336,2351,2363,2413,2723,2724,2725,2726,3730

Seq#:15; Xaa Pos. 1,2,3

VARIABLE LOCATION SUMMARY

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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 2320,2321,2336,2351,2363,2413,2723,2724,2725,2726,3730

Seq#:15; Xaa Pos. 1,2,3

VERIFICATION SUMMARY

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Input Set : N:\Crif3\Datahold\EFS\09936035\gncap01005.txt

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L:763 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:763 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2280
L:764 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:764 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340
L:765 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:765 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2400
L:770 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:770 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2700
L:787 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:787 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:3720
L:1119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0